

SEQUENCE LISTING

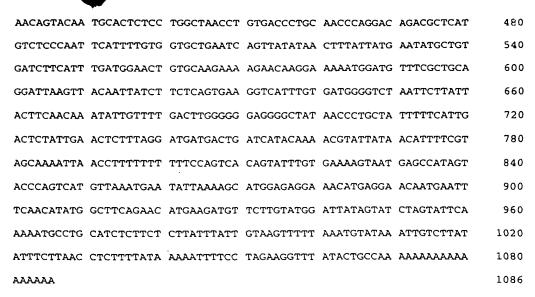
| (1 |) | GENERAL | INFORMATION |
|----|---|---------|-------------|
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- (i) APPLICANT: Bowman, Michael
- (ii) TITLE OF INVENTION: SECRETED PROTEIN BA3.1 AND POLYNUCLEOTIDES ENCODING SAME
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive

 - (C) CITY: Cambridge
 (D) STATE: Massachusetts
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Sprunger, Suzanne A.(B) REGISTRATION NUMBER: 41,323

 - (C) REFERENCE/DOCKET NUMBER: GI5295A
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 498-8284
 - (B) TELEFAX: (617) 876-5851
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1086 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| GCGGCGGT | AC GATTTGTTAG | ACACAGGAGA | TGATCTTGAC | CCTGATATCA | TTAATATCCT | 60 |
|----------|---------------|------------|------------|------------|------------|-----|
| TCCTGCTT | CT CCAACTGGTT | CTCCTGTACA | TTCTCCAGGA | TCTCATTACC | CCCATGGAGG | 120 |
| TGATGCGG | GC AAGGGTCAGA | GTACTGATCG | GCTACTATCA | ACAGAACCTC | ATGAGGAAGT | 180 |
| ACCTAATA | TT CTTCAGCAAC | CATTGGCCCT | TGGTTACTTT | GTATCAACTG | CCAAAGCAGG | 240 |
| TCCATTAC | CT GACTGGTTCT | GGTCAGCATG | TCCTCAAGCA | CAATATCAGT | GTCCCCTTTT | 300 |
| TTCTTAAG | GC CTCTTTGCAC | CTCCACGTGC | CTTCAGTGCA | ATCTGACGAG | CTGCTTCACA | 360 |
| GTAAACAC | TC CCACCCACTT | GACTCAAATC | AGACTTCAGA | TGTCCTCAGG | TTTGTTTTGG | 420 |



(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
- Met Ile Leu Thr Leu Ile Ser Leu Ile Ser Phe Leu Leu Cln Leu 1 5 10 15
- Val Leu Leu Tyr Ile Leu Gln Asp Leu Ile Thr Pro Met Glu Val Met $20 \hspace{1cm} 25 \hspace{1cm} 30$
- Arg Ala Arg Val Arg Val Leu Ile Gly Tyr Tyr Gln Gln Asn Leu Met 35 40 45
- Arg Lys Tyr Leu Ile Phe Phe Ser Asn His Trp Pro Leu Val Thr Leu 50 55 60
- Tyr Gln Leu Pro Lys Gln Val His Tyr Leu Thr Gly Ser Gly Gln His 65 70 75 80
- Val Leu Lys His Asn Ile Ser Val Pro Phe Phe Leu Lys Ala Ser Leu 85 90 95
- His Leu His Val Pro Ser Val Gln Ser Asp Glu Leu Leu His Ser Lys 100 105 110
- His Ser His Pro Leu Asp Ser Asn Gln Thr Ser Asp Val Leu Arg Phe 115 120 125
- Val Leu Glu Gln Tyr Asn Ala Leu Ser Trp Leu Thr Cys Asp Pro Ala 130 135 140
- Thr Gln Asp Arg Arg Ser Cys Leu Pro Ile His Phe Val Val Leu Asn 145 150 155 160
- Gln Leu Tyr Asn Phe Ile Met Asn Met Leu 165